

Martínez/Needleman-Wunsch DNA Alignment

Seq1(1>1984)

	Seq1(1>1984)	Seq2(1>1647)	Similarity	Gap	Gap Consensus
Seq1(1>1984)					
Seq2(1>1647)					
Similarity					
Gap					
Gap Consensus					

h5-HT6 GSDB S40337 flatfile

(333>1984)

(333>1984)

recession

No for gerban 5

v340	v350	v360
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ACTCACCTCCCGGGGGCGTGGTGAGTC

ACTCACCTCCCCCGGGCGTGGTGAGTC

ACTCACCTCCCCGGGGGGTGGTGAGTC

$$\wedge^{10} \quad \wedge^{20} \quad \wedge$$
[illegible]

v420	v430	v440
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CCATCATCTGCTTTCCGCCACCCCTATCACT

CCCTCATCTGCTTTCCCGCCACCCCTATCCTT

$$^{80} \quad ^{90} \quad ^{100}$$

223

v500	v510	v52
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CCAATAGCACCCGGCCTGGGGCAGGGC

CCAATAGCACCCGGCCTGGGGGCAGG C

CCAATAGCACCCGGCCTGGGGCAGG-C

$$^{\wedge}160 \quad ^{\wedge}170 \quad ^{\wedge}180$$

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0580 V590 V

GGTCAACGCTGACGGCGGCCCAACTC

591CAI CCGCI GACGGCGGCGGCGCAAC

$$^{240} \quad ^{250} \quad ^{260}$$

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v660	v670	v680
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AACTTCTTCCTGGTGCCTCTTCACGTCTC

AACTTCTTCCTGGTGTGCTCTTCACGTCCTC

AACTTCTTCCTGGTGTGCTCTTCACGTCCTC

^320 ^330 ^340 ^350 ^360 ^370 ^380 ^390
 v740 v750 v760 v770 v780 v790 v800 v810
 GTACGGCGCTGGGTGCTGGCGCGGCGCTCTGCCTGCTCGACCGCCTTCGACGTGATGTGCTGCAGCGCCTCCATCC
 GTACGGCGCTGGGTGCTGGCGCGGCGCTCTGCCTGCTCGACCGCCTTCGACGTGATGTGCTGCAGCGCCTCCATCC
 GTACGGCGCTGGGTGCTGGCGCGGCGCTCTGCCTGCTCGACCGCCTTCGACGTGATGTGCTGCAGCGCCTCCATCC
 ^400 ^410 ^420 ^430 ^440 ^450 ^460 ^470
 v820 v830 v840 v850 v860 v870 v880 v890
 TCAACCTCTGCCTCATCAGCCTGGACCGCTACCTGCTCATCTCTCGCGCTGCGCTACAAAGCTGGCATGACGCCCTG
 TCAACCTCTGCCTCATCAGCCTGGACCGCTACCTGCTCATCTCTCGCGCTGCGCTACAAAGCTGGCATGACGCCCTG
 TCAACCTCTGCCTCATCAGCCTGGACCGCTACCTGCTCATCTCTCGCGCTGCGCTACAAAGCTGGCATGACGCCCTG
 ^480 ^490 ^500 ^510 ^520 ^530 ^540 ^550
 v900 v910 v920 v930 v940 v950 v960 v970
 CGTGCCCTGGCCCTAGTCTCTGGCGCGCTGGAGCCTCGCGCTCTCGCCTCTTCTGCCCCCTGCTGGGCTGGCACGA
 CGTGCCCTGGCCCTAGTCTCTGGCGG CTGGAGCCTCGCGCTCTCGCCTCTTCTGCCCCCTGCTGGGCTGGCACGA
 CGTGCCCTGGCCCTAGTCTCTGGCGCGCTGGAGCCTCGCGCTCTCGCCTCTTCTGCCCCCTGCTGGGCTGGCACGA
 ^560 ^570 ^580 ^590 ^600 ^610 ^620 ^630
 v980 v990 v1000 v1010 v1020 v1030 v1040 v1050
 GCTGGGCCACGCACGGCCACCCGTCCCTGGCCAGTGCGCGCTGCTGGCCAGCCTGCTTTGTCTTGTGGCTGGGCC
 GCTGGGCCACGCACGGCCACCCGTCCCTGGCCAGTGCGCGCTGCTGGCCAGCCTGCTTTGTCTTGTGGCTGGGCC
 GCTGGGCCACGCACGGCCACCCGTCCCTGGCCAGTGCGCGCTGCTGGCCAGCCTGCTTTGTCTTGTGGCTGGGCC
 ^640 ^650 ^660 ^670 ^680 ^690 ^700 ^710
 v1060 v1070 v1080 v1090 v1100 v1110 v1120 v1130
 TCACCTTCTTCTGCCCCCTGCGGTGCCATATGCTTCACTACTGCAGGATCCTGCTAGTGGCCGCAAGCAGGCCGTGCAG
 TCACCTTCTTCTGCCCCCTGCGGTGCCATATGCTTCACTACTGCAGGATCCTGCTAGTGGCCGCAAGCAGGCCGTGCAG
 TCACCTTCTTCTGCCCCCTGCGGTGCCATATGCTTCACTACTGCAGGATCCTGCTAGTGGCCGCAAGCAGGCCGTGCAG
 ^720 ^730 ^740 ^750 ^760 ^770 ^780 ^790
 v1140 v1150 v1160 v1170 v1180 v1190 v1200
 GTGGCCCTCCCTCACCACCGCATGGCCAGTACGGCCCTCGGAGACGCTGCAGGTGCCAGGACCCACGCC-CAGGGGTGG
 GTGGCCCTCCCTCACCACCGCATGGCCAGTACGGCCCTCGGAGACGCTGCAGGT CCCAGGA CCCA GC CAGGGGTGG
 GTGGCCCTCCCTCACCACCGCATGGCCAGTACGGCCCTCGGAGACGCTGCAGGTACCCAGGAGCCCCA-GCGGCAGGGGTGG

^800 ^810 ^820 ^830 ^840 ^850 ^860 ^870
v1210 v1220 v1230 v1240 v1250 v1260 v1270 v1280
AGTCTGTGACAGCAGGGCTCTAGCCACGAAGCA-CAGCAGGAAGCCCTGAAGGCCAGCCTGACGCTGGGCATCCTGCT
AGTCTGTGACAGCAGGGCTCTAGC ACGAAG A CAGCAGGAAGG CCTGAAGGCCAGC TGACGCTGGGCATCCTGCT
AGTCTGTGACAGCAGGGCTCTAGCAACGAAG-AGCAGCAGGAAGGCCCTGAAGGCCAGCATGACGCTGGGCATCCTGCT
^880 ^890 ^900 ^910 ^920 ^930 ^940 ^950
v1290 v1300 v1310 v1320 v1330 v1340 v1350 v1360
GGGCATGTTCTTTGTGACCTGGTTGCCCTTCTTTGTGGCCAACATAGTCCAGGCCGTGTGGACTGCATCTCCCCAGGCC
GGGCATGTTCTTTGTGACCTGGTTGCCCTTCTTTGTGGCCAACATAGTCCAGGCCGTGTGGACTGCATCTCCCCAGGCC
GGGCATGTTCTTTGTGACCTGGTTGCCCTTCTTTGTGGCCAACATAGTCCAGGCCGTGTGGACTGCATCTCCCCAGGCC
^960 ^970 ^980 ^990 ^1000 ^1010 ^1020 ^1030
v1370 v1380 v1390 v1400 v1410 v1420 v1430 v1440
TCTTCGATGTCCTCACATGGCTGGTTACTGTAAACAGCACCATGAACCCCATCATCTACCCACTCTTTCATGCGGGACTTC
TCTTCGATGTCCTCACATGGCTGGTTACTGTAAACAGCACCATGAACCCCATCATCTACCCACTCTTTCATGC GGACTTC
TCTTCGATGTCCTCACATGGCTGGTTACTGTAAACAGCACCATGAACCCCATCATCTACCCACTCTTTCATGCTGGACTTC
^1040 ^1050 ^1060 ^1070 ^1080 ^1090 ^1100 ^1110
v1450 v1460 v1470 v1480 v1490 v1500 v1510 v1520
AAGCGGGCGCTGGCAGGTTCTTGCCATGTCCACGCTGTCCCGGGAGCGCCAGGCCAGCCTGGCCTCGCCATCACTGCG
AAGCGGGCGCTGGCAGGTTCTTGCCATGTCCACGCTGTCCCGGGAGC CCAGGCCAGCCTGGCCTCGCCATCACTGCG
AAGCGGGCGCTGGCAGGTTCTTGCCATGTCCACGCTGTCCCGGGAGC-CCAGGCCAGCCTGGCCTCGCCATCACTGCG
^1120 ^1130 ^1140 ^1150 ^1160 ^1170 ^1180 ^1190
v1530 v1540 v1550 v1560 v1570 v1580 v1590 v1600
CACCTCTACAGGGCCCCCGGCCCTTAGCCTACAGCAGGTGCTGCCGTGCCCTGCCCGGACTCAGATTTCGG
CACCTCTACAGGGCCCCCGGCCCTTAGCCTACAGCAGGTGCTGCCGTGCCCTGCCCGGACTCAGATTTCGG
CACCTCTACAGGGCCCCCGGCCCTTAGCCTACAGCAGGTGCTGCCGTGCCCTGCCCGGACTCAGATTTCGG
^1200 ^1210 ^1220 ^1230 ^1240 ^1250 ^1260 ^1270
v1610 v1620 v1630 v1640 v1650 v1660 v1670 v1680
ACTCAGACGAGGCTCAGGGGCTCCTCGGGCTGCGGCTCAGGCCCAGCTGCTGCTTCTGGCGAGGCCACCCAGGAC
ACTCAGACGAGGCTCAGGGGCTCCTCGGGC TCGGCTCAGGCCCAGCTGCTGCTTCTGGCGAGGCCACCCAGGAC
ACTCAGACGAGGCTCAGGGGCTCCTCGGGCTGCGGCTCAGGCCCAGCTGCTGCTTCTGGCGAGGCCACCCAGGAC

^1280 ^1290 ^1300 ^1310 ^1320 ^1330 ^1340 ^1350
 v1690 v1700 v1710 v1720 v1730 v1740 v1750 v1760
 CCCCCTGCCCCACGAGGCGCTGCCGCCGTCAATTCTTCAACATCG-ACCCCGCGGAGCCCGAGCTGCGGCCGCATC
 CCCCCTGCCCCACGAGGCGCTGCCGCCGTCAATTCTTCAACATCG ACCCCGCGGAGCCCGAGCTGCGGCCGCATC
 CCCCCTGCCCCACGAGGCGCTGCCGCCGTCAATTCTTCAACATCGSACCCCGCGGAGCCCGAGCTGCGGCCGCATC
 ^1360 ^1370 ^1380 ^1390 ^1400 ^1410 ^1420 ^1430
 v1770 v1780 v1790 v1800 v1810 v1820 v1830 v1840
 CACTTGGCATCCCCACGAACCTGACCCGGGCTTGGGCTGGCCAATGGGAGCTGGATTGAGCAGAACCCAGACCCCTGAGT
 CACTTGGCATCCCCACGAACCTGACCC GGCTTGGGCTGGCCAATGGGAGCTGGATTGAGCAGAACCCAGACCCCTGAGT
 CACTTGGCATCCCCACGAACCTGACCC-GGCTTGGGCTGGCCAATGGGAGCTGGATTGAGCAGAACCCAGACCCCTGAGT
 ^1440 ^1450 ^1460 ^1470 ^1480 ^1490 ^1500 ^1510
 v1850 v1860 v1870 v1880 v1890 v1900 v1910 v1920
 CCTTGGGCCAGCTCTTGGCTAAGACCAAGAGGCTGCAAGTCTCCTAGAAGCCCTCTGAGCTCCAGAGGGGTGCG-CAGAG
 CCTTGGGCCAGCTCTTGGCTAAGACCAAGAGGCTGCAAGTCTCCTAGAAGCCCTCTGAGCTCCAGAGGGGTGCG CAGAG
 CCTTGGGCCAGCTCTTGGCTAAGACCAAGAGGCTGCAAGTCTCCTAGAAGCCCTCTGAGCTCCAGAGGGGTGCGGCAGAG
 ^1520 ^1530 ^1540 ^1550 ^1560 ^1570 ^1580 ^1590
 v1930 v1940 v1950 v1960 v1970 v1980
 CTGACCCCTGCTGCCATCTCCAGGCCCTTACCTGCAGGGATCATAGCTGACTCAGA
 CTGACCCCTGCTGCCATCTCCAGGCCCTTACCTGCAGGGATCATAGCTGACT AGA
 CTGACCCCTGCTGCCATCTCCAGGCCCTTACCTGCAGGGATCATAGCTGACT-AGA
 ^1600 ^1610 ^1620 ^1630 ^1640

Lipman-Pearson Protein Alignment

Seq1(1>440) pep h5-HT6 GSDB S40337 Flafile PEP
Seq2(1>439) Seq ID¹ 13 - h 5-HT6 from application

(1>440)
(1>439)

Similarity

	Gap Number	Gap Length	Consensus Length
	5	5	442

v10	v20	v30	v40	v50	v60	v70	v80	v90	v100	v110	v120
MVPEPGTANSTPAWGAGPPSAPGGSGWVAALCVVIALTAANSLLIALLICTQPALRNTSNFFLVSLFTSDLMVGLVVMPPAMLNALYGRWVLARGCLLWTAFDVMCCSASILNLCII											
			:								
MVPEPGTANSTPAWGAGARXX-GGSGWVAAGLCVVIALTAANSLLIALLICTQPALRNTSNFFLVSLFTSDLMVGLVVMPPAMLNALYGRWVLARGCLLWTAFDVMCCSASILNLCII											
^10	^20	^30	^40	^50	^60	^70	^80	^90	^100	^110	
v130	v140	v150	v160	v170	v180	v190	v200	v210	v220	v230	v240
SLDRYLILSPRYKLRMTPLRALALVLGAWSLAALASFLPLLGWHELGHARPVPVGQCRLLASLPFVLVASGLTFFLPSCGAICFTYCRILLAAARKQAVQVASLTGTGMASQASETLQVP											
			:								
SLDRYLILSPRYKLRMTPLRALALVLGWSLAALASFLPLLGWHELGHARPVPVGQCRLLASLPFVLVASGLTFFLPSCGAICFTYCRILLAAARKQAVQVASLTGTGMASQASETLQVP											
^120	^130	^140	^150	^160	^170	^180	^190	^200	^210	^220	^230
v250	v260	v270	v280	v290	v300	v310	v320	v330	v340	v350	v360
RTRPRPVGESADSRRLATKHRSRKALKASLTGLIGMFFVTWLPPFFVANIVQAVCDICISPGLFVDLTWLGYCNSTMNPPIIYPLFMDFKRALGRFLPCPRCPRERQASLASPSLRTSHSGP											
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RSIPAAGESADSRRLATKSSPKGLKASMTLIGLIGMFFVTWLPPFFVANIVQAVCDICISPGLFVDLTWLGYCNSTMNPPIIYPLFMDFKRALGRFLPCPRCPRERQASLASPSLRTSHSGP											
^240	^250	^260	^270	^280	^290	^300	^310	^320	^330	^340	^350